

PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/744,852

DATE: 04/25/2001

TIME: 07:30:53

Input Set : A:\es.txt

Output Set: N:\CRF3\04252001\I744852.raw

ENTERED

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3 <110> APPLICANT: FROHBERG, Claus
5 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING A-AMYLASE, PLANTS WHICH
SYNTHESIZE A
6     MODIFIED STARCH, GENERATION PROCESSES AND USES
8 <130> FILE REFERENCE: 514413-3864
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/744,852
C--> 10 <141> CURRENT FILING DATE: 2001-01-30
10 <150> PRIOR APPLICATION NUMBER: PCT/EP99/05523
11 <151> PRIOR FILING DATE: 1999-07-30
13 <150> PRIOR APPLICATION NUMBER: 198 36 099.1
14 <151> PRIOR FILING DATE: 1998-07-31
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn version 3.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1950
22 <212> TYPE: DNA
23 <213> ORGANISM: Solanum tuberosum
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (16)..(1752)
28 <223> OTHER INFORMATION: coding sequence beta-amylase
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33           Met Ala Met Ser Leu Pro His Gln Ile Gly Ala Leu
34           1             5             10
36 tca gga aca tcg ctc acg gcg gaa acc ggt gga gtt tca tgc gaa gtt      99
37 Ser Gly Thr Ser Leu Thr Ala Glu Thr Gly Gly Val Ser Cys Glu Val
38     15             20             25
40 ccg gcg aag ggg agt tca gct aca tca gct atg tgg aga aca ccg atg      147
41 Pro Ala Lys Gly Ser Ser Ala Thr Ser Ala Met Trp Arg Thr Pro Met
42     30             35             40
44 acg aat tta aaa gta tcg gta caa aaa aca gga act gaa att gac agg      195
45 Thr Asn Leu Lys Val Ser Val Gln Lys Thr Gly Thr Glu Ile Asp Arg
46 45             50             55             60
48 gtg tcg ccg tcg ccg tcg ccg ccg atg agt ccg atg atg gga gga gga      243
49 Val Ser Pro Ser Pro Ser Pro Pro Met Ser Pro Met Met Gly Gly Gly
50           65             70             75
52 atg cgg ccg gat tta tta gcg tgt caa gcg ttg atg gaa gct cag gta      291
53 Met Arg Pro Asp Leu Leu Ala Cys Gln Ala Leu Met Glu Ala Gln Val
54           80             85             90
56 gat gag gta gtt gag aga gaa tat aag gtt agg aat tcg tcg gag aaa      339
57 Asp Glu Val Val Glu Arg Glu Tyr Lys Val Arg Asn Ser Ser Glu Lys
58           95             100            105
60 gag aaa gga gtt ccg gtg ttt gtt atg atg ccg ttg gat agt gtg aaa      387
61 Glu Lys Gly Val Pro Val Phe Val Met Met Pro Leu Asp Ser Val Lys
62     110            115            120
64 atg gat cat act gtg aat agg aag aag gcg atg aat gcg agt tta cag      435
65 Met Asp His Thr Val Asn Arg Lys Lys Ala Met Asn Ala Ser Leu Gln

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66	125					130				135					140		
68	gcg	tta	aag	agc	gcc	ggt	gtg	gaa	ggg	att	atg	atg	gat	gtg	tgg	tgg	483
69	Ala	Leu	Lys	Ser	Ala	Gly	Val	Glu	Gly	Ile	Met	Met	Asp	Val	Trp	Trp	
70					145					150					155		
72	gga	tta	gtg	gag	aga	gat	gcg	ccg	gga	gag	tat	aat	tgg	ggc	ggt	tat	531
73	Gly	Leu	Val	Glu	Arg	Asp	Ala	Pro	Gly	Glu	Tyr	Asn	Trp	Gly	Gly	Tyr	
74				160					165					170			
76	gct	gag	ctt	atg	gaa	atg	gcg	aaa	aaa	cat	gga	ctc	aaa	gtt	caa	gct	579
77	Ala	Glu	Leu	Met	Glu	Met	Ala	Lys	Lys	His	Gly	Leu	Lys	Val	Gln	Ala	
78			175					180					185				
80	gtg	atg	tct	ttc	cat	caa	tgt	ggt	gga	aac	gtc	ggt	gat	tcc	tgc	acg	627
81	Val	Met	Ser	Phe	His	Gln	Cys	Gly	Gly	Asn	Val	Gly	Asp	Ser	Cys	Thr	
82		190					195				200						
84	atc	cct	ctt	cca	agg	tgg	gtt	gtt	gag	gag	atg	gag	aag	gat	cca	gat	675
85	Ile	Pro	Leu	Pro	Arg	Trp	Val	Val	Glu	Glu	Met	Glu	Lys	Asp	Pro	Asp	
86	205				210					215					220		
88	ctt	gca	tac	aca	gat	cag	tgg	gga	agg	agg	aat	ttt	gaa	tat	gta	tcg	723
89	Leu	Ala	Tyr	Thr	Asp	Gln	Trp	Gly	Arg	Arg	Asn	Phe	Glu	Tyr	Val	Ser	
90				225					230					235			
92	ctt	ggt	tgc	gat	aca	ctt	cca	gtt	ctt	aaa	gga	agg	act	cct	gtc	caa	771
93	Leu	Gly	Cys	Asp	Thr	Leu	Pro	Val	Leu	Lys	Gly	Arg	Thr	Pro	Val	Gln	
94			240					245					250				
96	tgc	tat	tct	gat	ttc	atg	aga	ggg	ttt	aga	gat	aga	ttt	gag	aat	ctc	819
97	Cys	Tyr	Ser	Asp	Phe	Met	Arg	Gly	Phe	Arg	Asp	Arg	Phe	Glu	Asn	Leu	
98		255					260				265						
100	cta	ggt	gac	acc	att	gtg	gaa	att	caa	gtc	ggg	atg	ggt	cca	gct	gga	867
101	Leu	Gly	Asp	Thr	Ile	Val	Glu	Ile	Gln	Val	Gly	Met	Gly	Pro	Ala	Gly	
102		270				275				280							
104	gag	ctc	cgt	tat	cca	tcc	tat	ccg	gaa	aaa	gat	gga	gta	tgg	aaa	ttc	915
105	Glu	Leu	Arg	Tyr	Pro	Ser	Tyr	Pro	Glu	Lys	Asp	Gly	Val	Trp	Lys	Phe	
106	285				290				295					300			
108	cct	gga	att	ggt	gct	ttt	cag	tgt	tat	gac	aag	tac	atg	atc	agt	agc	963
109	Pro	Gly	Ile	Gly	Ala	Phe	Gln	Cys	Tyr	Asp	Lys	Tyr	Met	Ile	Ser	Ser	
110			305				310						315				
112	tta	cag	ggt	gca	gca	gaa	gct	ttt	ggt	aag	cct	gaa	tgg	gga	cac	acc	1011
113	Leu	Gln	Gly	Ala	Ala	Glu	Ala	Phe	Gly	Lys	Pro	Glu	Trp	Gly	His	Thr	
114			320														

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132 gtt aag att gca ggt att cac tgg cac tat gga aca agg tcc cat gcc      1251
133 Val Lys Ile Ala Gly Ile His Trp His Tyr Gly Thr Arg Ser His Ala
134      400      405      410
136 cct gag ctg acc gct gga tac tac aac acc cgt aac cga gat ggt tac      1299
137 Pro Glu Leu Thr Ala Gly Tyr Tyr Asn Thr Arg Asn Arg Asp Gly Tyr
138      415      420      425
140 ctt ccc atc gcc caa atg ctt gcc cgc cac ggt gca gtt ttc aac ttc      1347
141 Leu Pro Ile Ala Gln Met Leu Ala Arg His Gly Ala Val Phe Asn Phe
142      430      435      440
144 aca tgt gtt gag atg cgt gac cac gag cag cca caa gat gca cta tgt      1395
145 Thr Cys Val Glu Met Arg Asp His Glu Gln Pro Gln Asp Ala Leu Cys
146 445      450      455      460
148 gca cct gag aag ttg gtt agg caa gtg gct tta gca act cag gaa gct      1443
149 Ala Pro Glu Lys Leu Val Arg Gln Val Ala Leu Ala Thr Gln Glu Ala
150      465      470      475
152 caa gtt cca ctt gct ggg gag aat gca ttg cca cga tac gat gat tat      1491
153 Gln Val Pro Leu Ala Gly Glu Asn Ala Leu Pro Arg Tyr Asp Asp Tyr
154      480      485      490
156 gca cat gaa cag atc ctt caa gca tcc tca ttg aat atc aac gat caa      1539
157 Ala His Glu Gln Ile Leu Gln Ala Ser Ser Leu Asn Ile Asn Asp Gln
158      495      500      505
160 tca ggt gat aga gag atg tgc gcg ttt aca tat ttg agg atg aat cct      1587
161 Ser Gly Asp Arg Glu Met Cys Ala Phe Thr Tyr Leu Arg Met Asn Pro
162      510      515      520
164 gac cta ttc cat cct gat aac tgg agg cga ttc gtt gcc ttc gtg aag      1635
165 Asp Leu Phe His Pro Asp Asn Trp Arg Arg Phe Val Ala Phe Val Lys
166 525      530      535      540
168 aaa atg aaa gaa gga aaa gac gca aac aaa tgc cgg gaa caa gta gag      1683
169 Lys Met Lys Glu Gly Lys Asp Ala Asn Lys Cys Arg Glu Gln Val Glu
170      545      550      555
172 agg gag gca gag cat ttc gtg cat ata act cag ccg tta gtg caa gaa      1731
173 Arg Glu Ala Glu His Phe Val His Ile Thr Gln Pro Leu Val Gln Glu
174      560      565      570
176 gct gca gct gcc ctc atg cac taagcaaatg gttgtcaaat agtactgtaa      1782
177 Ala Ala Ala Leu Met His
178      575
180 ttttgatcct ttttagctaac atggagtttt tcaacatggtt acgaggatct tatagctcgt      1842
182 tatcgttctt cttatatggt tgtaaaactg tccatcgtgt attttttcga agttagacat      1902
184 tatgtcttaa tgaaatgata cataattcag tagtaaaaaa aaaaaaaa      1950
187 <210> SEQ ID NO: 2
188 <211> LENGTH: 579
189 <212> TYPE: PRT
190 <213> ORGANISM: Solanum tuberosum
192 <400> SEQUENCE: 2
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195 1      5      10      15
198 Leu Thr Ala Glu Thr Gly Gly Val Ser Cys Glu Val Pro Ala Lys Gly
199      20      25      30
202 Ser Ser Ala Thr Ser Ala Met Trp Arg Thr Pro Met Thr Asn Leu Lys

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203		35				40			45					
206	Val	Ser	Val	Gln	Lys	Thr	Gly	Thr	Glu	Ile	Asp	Arg	Val	Ser
207		50					55					60		
210	Pro	Ser	Pro	Pro	Met	Ser	Pro	Met	Met	Gly	Gly	Gly	Met	Arg
211	65					70					75			80
214	Leu	Leu	Ala	Cys	Gln	Ala	Leu	Met	Glu	Ala	Gln	Val	Asp	Glu
215					85					90				95
218	Glu	Arg	Glu	Tyr	Lys	Val	Arg	Asn	Ser	Ser	Glu	Lys	Glu	Lys
219				100					105				110	
222	Pro	Val	Phe	Val	Met	Met	Pro	Leu	Asp	Ser	Val	Lys	Met	Asp
223			115					120					125	
226	Val	Asn	Arg	Lys	Lys	Ala	Met	Asn	Ala	Ser	Leu	Gln	Ala	Leu
227		130					135					140		
230	Ala	Gly	Val	Glu	Gly	Ile	Met	Met	Asp	Val	Trp	Trp	Gly	Leu
231	145					150					155			160
234	Arg	Asp	Ala	Pro	Gly	Glu	Tyr	Asn	Trp	Gly	Gly	Tyr	Ala	Glu
235					165					170				175
238	Glu	Met	Ala	Lys	Lys	His	Gly	Leu	Lys	Val	Gln	Ala	Val	Met
239				180					185				190	
242	His	Gln	Cys	Gly	Gly	Asn	Val	Gly	Asp	Ser	Cys	Thr	Ile	Pro
243			195					200					205	
246	Arg	Trp	Val	Val	Glu	Glu	Met	Glu	Lys	Asp	Pro	Asp	Leu	Ala
247		210					215					220		
250	Asp	Gln	Trp	Gly	Arg	Arg	Asn	Phe	Glu	Tyr	Val	Ser	Leu	Gly
251	225					230					235			240
254	Thr	Leu	Pro	Val	Leu	Lys	Gly	Arg	Thr	Pro	Val	Gln	Cys	Tyr
255					245					250				255
258	Phe	Met	Arg	Gly	Phe	Arg	Asp	Arg	Phe	Glu	Asn	Leu	Leu	Gly
259			260						265				270	
262	Ile	Val	Glu	Ile	Gln	Val	Gly	Met	Gly	Pro	Ala	Gly	Glu	Leu
263		275					280						285	
266	Pro	Ser	Tyr	Pro	Glu	Lys	Asp	Gly	Val	Trp	Lys	Phe	Pro	Gly
267		290					295					300		
270	Ala	Phe	Gln	Cys	Tyr	Asp	Lys	Tyr	Met	Ile	Ser	Ser	Leu	Gln
271	305					310					315			320
274	Ala	Glu	Ala	Phe	Gly	Lys	Pro	Glu	Trp	Gly	His	Thr	Gly	Pro
275					325					330				335
278	Ala	Gly	Gln	Tyr	Asn	Asn	Trp	Pro	Glu	Asp	Thr	Asn	Phe	Phe
279				340					345					350
282	Glu	Gly	Gly	Gly	Trp	Asp	Ser	Gln	Tyr	Gly	Glu	Phe	Phe	Leu
283		355						360					365	
286	Tyr	Ser	Glu	Met	Leu	Leu	Asn	His	Gly	Glu	Arg	Ile	Leu	Gln
287		370					375					380		
290	Lys	Ala	Ile	Phe	Glu	Asp	Lys	Gly	Val	Lys	Ile	Ser	Val	Lys
291	385					390					395			400
294	Gly	Ile	His	Trp	His	Tyr	Gly	Thr	Arg	Ser	His	Ala	Pro	Glu
295					405					410				415
298	Ala	Gly	Tyr	Tyr	Asn	Thr	Arg	Asn	Arg	Asp	Gly	Tyr	Leu	Pro
299				420					425					430

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302 Gln Met Leu Ala Arg His Gly Ala Val Phe Asn Phe Thr Cys Val Glu
303      435      440      445
306 Met Arg Asp His Glu Gln Pro Gln Asp Ala Leu Cys Ala Pro Glu Lys
307      450      455      460
310 Leu Val Arg Gln Val Ala Leu Ala Thr Gln Glu Ala Gln Val Pro Leu
311 465      470      475      480
314 Ala Gly Glu Asn Ala Leu Pro Arg Tyr Asp Asp Tyr Ala His Glu Gln
315      485      490      495
318 Ile Leu Gln Ala Ser Ser Leu Asn Ile Asn Asp Gln Ser Gly Asp Arg
319      500      505      510
322 Glu Met Cys Ala Phe Thr Tyr Leu Arg Met Asn Pro Asp Leu Phe His
323      515      520      525
326 Pro Asp Asn Trp Arg Arg Phe Val Ala Phe Val Lys Lys Met Lys Glu
327      530      535      540
330 Gly Lys Asp Ala Asn Lys Cys Arg Glu Gln Val Glu Arg Glu Ala Glu
331 545      550      555      560
334 His Phe Val His Ile Thr Gln Pro Leu Val Gln Glu Ala Ala Ala Ala
335      565      570      575
338 Leu Met His

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VERIFICATION SUMMARY

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L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date